

REMARKS

In the Office Action mailed September 14, 2006, the Examiner has required an election of one of the following inventions:

- I. Claims 122 and 185-232, drawn to arrays of polynucleotides, classified in class 435, subclass 40.5; and
- II. Claim 178, drawn to a method for preparing an array of polynucleotides, classified in class 536, subclass 25.3.

The Examiner contends that inventions I and II are distinct. If invention I is elected, the Examiner has required a further election of one species for each of array range, probe proximity, probe size and proximity, and first plurality of probes, as follows:

- 1. Array range
 - a. 150 to 1,000 different polynucleotides per cm² (claim 186 in part);
 - b. 1,000 to 10,000 different polynucleotides per cm² (claim 187 in part);
 - c. 10,000 to 50,000 different polynucleotides per cm² (claim 188 in part); or
 - d. greater than 50,000 polynucleotides per cm² (claim 189 in part).
- 2. Probe Proximity
 - a. genomic sequences for different probes are overlapping (claim 190 in part);
 - b. genomic sequences for different probes are adjacent (claim 191 in part);
or
 - c. genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 192 in part).
- 3. Probe Size and Proximity
 - a. nucleotide sequences of probes are no more than 1,000 nucleotides (claim 193 in part);

- i) genomic sequences for different probes are overlapping (claim 194 in part);
 - ii) genomic sequences for different probes are adjacent (claim 195 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 196 in part).
- b. nucleotide sequences of probes are 10-200 nucleotides (claim 197 in part)
 - i) genomic sequences for different probes are overlapping (claim 198 in part);
 - ii) genomic sequences for different probes are adjacent (claim 199 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 200 in part).
- c. nucleotide sequences of probes are 10-30 nucleotides (claim 201 in part)
 - i) genomic sequences for different probes are overlapping (claim 202 in part);
 - ii) genomic sequences for different probes are adjacent (claim 203 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 204 in part).
- d. nucleotide sequences of probes are 20-50 nucleotides (claim 205 in part)
 - i) genomic sequences for different probes are overlapping (claim 206 in part);
 - ii) genomic sequences for different probes are adjacent (claim 207 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 208 in part).

- e. nucleotide sequences of probes are 40-80 nucleotides (claim 209 in part)
 - i) genomic sequences for different probes are overlapping (claim 210 in part);
 - ii) genomic sequences for different probes are adjacent (claim 211 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 212 in part).
- f. nucleotide sequences of probes are 50-150 nucleotides (claim 213 in part)
 - i) genomic sequences for different probes are overlapping (claim 214 in part);
 - ii) genomic sequences for different probes are adjacent (claim 215 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 216 in part).
- g. nucleotide sequences of probes consist of 60 nucleotides (claim 217 in part)
 - i) genomic sequences for different probes are overlapping (claim 218 in part);
 - ii) genomic sequences for different probes are adjacent (claim 219 in part); or
 - iii) genomic sequences for each probe are set apart from other probes by less than 200 bp (claim 220 in part).

4. First Plurality of Probes

- a. is at least 1,000 probes (claim 225 in part);
- b. is at least 10,000 probes (claim 226 in part); or
- c. is in the range 1,000 to 50,000 probes (claim 227 in part).

In order to be fully responsive to the Examiner's requirement for a restriction of the instant application, Applicants hereby provisionally elect with traverse to prosecute invention I, claims 122 and 185-232, drawn to arrays of polynucleotides, classified in class 435, subclass 40.5.

With respect to the Examiner's requirement of an election of one species for Array Range, Applicants hereby provisionally elect with traverse to prosecute species d, greater than 50,000 polynucleotides per cm². Claims 122, 185, and 189-232 are believed to be readable upon the elected species.

With respect to the Examiner's requirement of an election of one species for Probe Proximity, Applicants hereby provisionally elect with traverse to prosecute species c, genomic sequences for each probe are set apart from other probes by less than 200 bp. Claims 122, 185-189, and 192-232 are believed to be readable upon the elected species.

With respect to the Examiner's requirement of an election of one species for Probe Size and Proximity, Applicants hereby provisionally elect with traverse to prosecute species b, nucleotide sequences of probes are 10-200 nucleotides, and iii), genomic sequences for each probe are set apart from other probes by less than 200 bp. Claims 122, 185-192, 200, and 221-232 are believed to be readable upon the elected species.

With respect to the Examiner's requirement of an election of one species for First Plurality of Probes, Applicants hereby provisionally elect with traverse to prosecute species b, at least 10,000 probes. Claims 122, 185-224, 226, and 228-232 are believed to be readable upon the elected species.

Claims 122, 185, 221-224, and 228-232 are believed to be generic to all elected species.

Entry and consideration of the foregoing remarks are respectfully requested.

Respectfully submitted,

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Adriane Antler *by* 32,605
Adriane M. Antler (Reg. No.)
JONES DAY *William Wang*
222 East 41st Street
New York, New York 10017-6702 *Ref. No. 47,164*
Phone: (212) 326-3939